Figure 1.

CCCGGTCGGAGGTTTCAAGGAATGACTAGATGTGGCACTTAGTGCCATGGTCTAGTTGAC	60
AAGGTGATGGTTGGTCAAAAGTTGGACTCGATGATCTCAGAGTTTTTTTCCAGCCTTAAT	120
AATTCTATGAATTCTGTAATTTTATTCTTGATCTTTTTGAGCGAAGTTTGTTT	180
TTAGTTTGGTTTCCCTGTCACTGTTTTCTTTCCTTGAAACTGACTTTCATTTGCAACATG	240
AGAATTGCTGTATTTGTCAGGTTACAAGTAGTGCAATGGCTGCTTAGAAGTAGTGAGAAA	300
CATTTAGGGAAATACTGGAGTGAAGCAAACACAGTGGTACTGCCAAACTGTAGCTTTGGG	360
ATTTGAGGAGCCACAGAGTTGTATATAAATTTGTTTAATGATATCCTGCCCTGCCTTCC	420
ATTAATTGCTTGTTTTATGAAACCACTCTTTTTTTTTTT	480
TATCCTGTGGTAATGAGTTAATGCATTTAGAAGCACATGGCAGAACTAGGAGATCTGTGG	540
ATGACAGTGGTACAGGAGCTCTGAATTTTTTAGATAAACTATGAGAGTGGAAACAGAAAT	600
CTGAGGCTAGTTTCTTGAGCTGACTGTAAATTTTGTGAGAATATTTTCAAGACTACATTA	660
GTTGTGTGTTTGAGGAAAAATAAAATGTTTAAGTTGTCCATTCCTTGAAACCTCCCGACC	720
GGG	723

Figure 2.

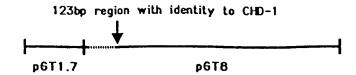
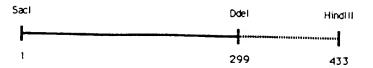


Figure 3.

M C C GT	CHD-1 CHD-1A CHD-W CHD-W	ATTTTACCTG ATTTTACCTG	ATGATCCTGA ATGATCCAGA ATGATCCAGA ATGACCCAGA	CAAGAAACCC TAAGAAACCC	CAGGCAAAGC CAGGCTAAGC	AGCTACAGAC AGTTACAGAC	
M C C GT	CBD-1 CBD-1A CBD-W CBD-W	CAAGAAACCC CAAGAAACCC	CAAGCAAAAC CAGGCAAAGC CAGGCTAAGC CAGGCAAAGC	AGCTACAGAC AGTTACAGAC	CCGTGCAGAC CCGTGCAGAT	TACCTCATTA TACCTCATTA	
M C C GT	CHD-1 CHD-1A CHD-W CHD-W	AATTACTGAA AATTACTGAA	CAGAGATCTT TAAAGACCTT TAAAGACCTT TAAAGACCTT	GCAAGAAAGG GCAAGAAAGG	AAGCACAAAG	GCTTGCTGGT ACTTGCTGGT	GCA GCA GCA
M C C GT	CHD-1 CHD-1A CHD-W CHD-W	IL:	PDDPDKKPQ# PDDPDKKPQ#	KQLQTRADY KQLQTRADY	LIKLLNKDLA LIKLLNKDLA	AKREAQRLCG ARKEAQRLAG ARKEAQRLAG ARKEVQRLTG	A

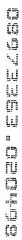
Figure 4.



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Figure 5.

_1		ACCGCCGGCC	CACGCAGGCT	CGGGCCGGC
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3001	AGAAGATGGT	GCTAGACCAT	TTAGTAATTC	AGAGAATGGA	CACGACAGGA
3051	AAAACTGTTC	TGCATACAGG	TTCAACTCCA	TCAAGCTCTA	CACCTTTTAA
3101	TAAAGAAGAG	TTATCAGCTA	TTTTGAAGTT	TGGTGCTGAG	GAACTCTTTA
3151	AAGAACCTGA	AGGAGAAGAA	CAGGAGCCCC	AGGAAATGGA	TATAGATGAA
3201	ATCTTGAAGA	GAGCTGAAAC	TCGGGAAAAT	GAGCCAGGTC	CATTGACTGT
3251	AGGGGATGAG	TTGCTTTCAC	AGTTCAAGGT	GGCGAACTTT	TCCAATATGG
3301	ATGAAGATGA	TATTGAGTTG	GAACCAGAAA	GAAATTCAAG	AAATTGGGAA
3351 3401	GAAATCATCC AAAAGAACTT	CAGAATCCCA		ATAGAGGAGG	AGGAAAGACA
3451	AACAGATCAG	GAAGAAATAT CTTTAATGGG	ACATGCTCCC AGTGAAGGAA	GAGGATGAGA	AACTGTGCAA
3501	TATTCTGGAT	CTGATAGTGA		GACGCAGTAG GAAAGAAAAC	GAGCAGAAAA GGCCAAAAAA
3551	GCGTGGAAGA	CCTCGAACCA	TTCCTCGAGA	AAATATTAAA	GGATTTAGTG
3601	ATGCAGAGAT	CAGGCGGTTT	ATCAAGAGTT	ACAAGAAATT	TGGTGGCCCT
3651	CTGGAAAGGT	TAGATGCTGT	AGCTAGAGAT	GCTGAACTGG	TTGATAAATC
3701	TGAGACAGAC	CTTAGACGTT	TGGGTGAACT	TGTACATAAT	GGATGCATTA
3751		GGACAATTCA	TCTGGACAAG	AAAGAGCAGG	AGGTAGACTT
3801	GGGAAAGTTA	AAGGCCCAAC	GTTTCGAATC	TCAGGAGTGC	AGGTGAATGC
3851	AAAACTAGTC	ATCTCTCACG	AAGAAGAGCT	GGCACCACTG	CACAAATCCA
3901	TTCCTTCAGA	TCCAGAAGAA	AGGAAAAGAT	ATGTCATCCC	ATGCCACACC
3951 4001	AAGGCTGCTC GTTAGTAGGC	ACTTCGATAT ATCTATGAAT	AGATTGGGGT	AAAGAAGATG	ATTCCAATCT
4051	TGGATCCAGA	TCTCAGCTTA	ATGGCTATGG ACACAGAAGA	CAGCTGGGAA TTTTACCTGA	ATGATAAAA
4101	AAGAAACCCC	AGGCAAAGCA	GCTACAGACC	CGTGCAGACT	TGATCCAGAC ACCTCATTAA
4151	ATTACTGAAT	AAAGACCTTG	CAAGAAAGGA		CTTGCTGGTG
4201	CAGGCAATTC	CAAGAGAAGG	AAGACAAGAA		TAAGATGAAG
4251	GCTTCAAAAA	TAAAAGAAGA	AATAAAGAGT	GATTCTTCAC	CACAACCCTC
4301	AGAAAAATCT	GATGAAGATG	ATGAGGAGGA	GGATAACAAG	GTAAATGAAA
			**		•
4351		AAATAAAGAA	AAATCTAAAA	AAATTCCATT	GCTGGATACT
4401	CCAGTTCATA	TTACTGCAAC	CAGTGAACCA		CAGAAGAATC
4451	TGAAGAACTC	CATCAGAAGA		GTGCAAAGAA	AGAATGAGGC
4501 4551	CTGTCAAAGC GAAAGGGAGC	AGCACTGAAA AGCTGGAACA	TACTAGGCAG	GACCAGAGAA	GGGCCTTTCT
4601	TCACATTACA		AGGAGTACAC	TGTCTAATCA AAATCCCGAG	AAATTGGGGA
4651		AAATTTGTGG	ATTTTTGTGT	CCAAGTTTAC	CAAATAAAAC AGAATTTGAT
4701	GCCAGAAAGC	TGCACAAACT	CTACAAACAT	GCAATCAAAA	AGCGCCAAGA
4751	GTCTCAGCAA	CACAATGACC	AAAACATTAG	CAGCAATGTG	AATACACATG
4801	TAATCAGAAA	TCCAGATGTG	GAAAGACTGA	-	AAACCATGAT
4851		GGGACAGTTA	TTCTTCTGAT	AGACATTTAT	CACAATACCA
4901		AAAGACAGGC	ATCAGGGAGA	TGCTTACAAG	AAAAGTGACT
4951	CCAGGAAAAG	GCCATATTCA	GCCTTCAGTA	ATGGAAAAGA	TCACAGAGAC
5001	TGGGATCACT	ACAAACAGGA		TACAGTGATA	GTAAACATAG
5051 5101	AAAGTTAGAT	GACCACAGGA			CTGGAAGGAA
5151		CAGCCGGGGT	TTCCACATC	ACCGCTCCCA GAATACAGCC	TTCAGACCAC
5201		TATAGATACC	ACTUAGACTG	GCAAATGGAC	CACAGAGCTT
5251			CCACTAGATC	AGAGGTCTCC	TTATGGTTCA
5301	AGATCTCCCC	TAGGACACAG	ATCTCCATTT	GAACACTCAT	CAGATCACAA
5351	AAGTACACCT	GAACATACAT	GGAGTAGCCG	GAAGACA <u>TAA</u>	CAAAGACTGA
5401	CATTTTCTGG	ACCTTCTTTT	TAGCCATATA	CAGTAAACTA	ACACAGTAAT
5451	TGCCTTACAT	GACTTGAAAG	ATATGGACTG	GATATTCTAT	CAGTAGCAGT
5501	ATTGTTACTT	CTTTCCAGGA	TGCAAGGTCT	ATTATCCCAA	CAGAAGAAAA
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5701				AACTCTTCAT TGTAAATGAA	
5751	CTGACCTGTG	CTTATGTTTC	ACCAAACAAT	GGGGGATTTA	TTTTTTTTT
5801				TTCACTTTCC	
5851				GCTTTTCATC	
5901	ATATTTAAAT	TCTGTACCTA	CAGTTGTAAA	ATAGCCAGGA	TTTCTCCTGT
5951	TTGTGATCAG	TTATAATGCC	TTTTTATGAA	ACAAACAAAC	AAACAAAAA
6001	CAATTAAAAA	AAAAAACACA	ACAAAACCAA	CAAATGGCTG	TAAATTATTG
6051	TAAATTAATT	AAATGAGCTT	TTTTCCGTCA	GGCTTTTTTT	GGCTGTTCCT
6101	TTCCCCAACA	ACTCAGGCCT	TCTTTTCACA	AAGTCAGTAT	ACTTACATGT
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6401	ACACTTCAAA	ACCCAGATCA	GCCAAGATTC	ATTGTAAATC	CATTTGTTTT
6451	CCCTCTTTAA	CATGGGCAAT	AATGTCAAAT	GTGCTATGCA	GC A GTTA A TA
6501	TTTTAGAAGA	TTTGAATGAC	TTTATTAACA	GAATTGTTAC	AATGCACACT
6551	GATTGTACAT	AGATAACTTC	TATCTGACAA	ATTAAATTAA	CTAAAACCAA
6601	AAAAAACC				CITEBRACCAA

Figure 6.

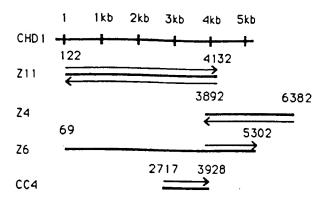


Figure 7.

DEIVSVKHLHKKIKTE CHD-1A 1 CHD-W GATGGGATTGTTTCAGTGAAACATCCACATAAAAAAATAAAAGCAGAAA DGIVSVKHPHKKIKAE K E N E E K P E P D I G I K K E A CHD-1A 51 CHD-W KENEEKDEPEIGIKKEA EEKRETKEKENKRELKR CBD-1A 101 GAAGAAAAAGAGAGACAAAAGAGAAAGGAAAATAAAAGGGAATTGAAAAGG GGAGAAAAAGAGAGACAAAAGAAAAGGAAAATAAGA GEKRETKEKENK K K E K E D K K E L K E K D N K CHD-1A 151 EKRENKVKESTQKEKEV KEEK CBD-1A 251 AAGGAAGAGAAG

Figure 8.

ATTTATCGGC	TAGTCACAAA	AGGATCAGTA	GAAGAAGATA	TTCTTGAAAG	AGCCAAGAAA	AAGATGGTGT	TAGATCATTT
. 10	20	30	40	50	60	70	80
AGTGATTCAG	AGAATGGACA	CCACAGGGAA	AACTGTACTA	CATACAGGCT	CTACTCCTTC	AAGCTCAACA	CCTTTTAATA
90	100	110	120	130	140	150	160
AGGAAGAGTT	ATCAGCAATT	TTGAAGTTTG	GTGCTGAGGA	ACTITITAAA	GAACCTGAAN	NNGAAGAAGA	GGAGCCTCAG
170	180	190	200	210	220	230	240
GAGATGGATA	TAGATGAAAT	CCTGAAGAGG	NCTGAAACTC	GAGAAAATGA	GTCAGGCCCA	TTANCTGTAG	GAGATGAGTT
250	260	270	280	290	300	310	320
			CANTATGGAT	GAAGATGACA	TTGAATTGGA	ACCAGAACAA	AATCTAAGAA
330	340	350	360	370	380	390	400
				AGAGGGGNING	GAAAGACAAA	AAGAACTTGA	AGAAATATAT
410	420	430	440	450	460	470	480
				TTAATGGAAA	TGAAGGGAGA	TGCAGTAGGA	GCAGAAGATA
490	500	510	520	530	540	550	560
			AAGAAAACGA	CCAAAAAAAC	GTGGACGACC	ACGAACTATT	CCCCGTGAAA
570	580	590	600	610	620	630	640
			GACGATTTAT	CAAGAGTTAC	AAGAAATTTG	GTGGCCCAGT	TGAAAGGTTA
650	660	670	680	690	700	710	720
	CTAGAGATGC	TGAGCTAGTT	GATAAATCTG	AAACAGACCT	TAGACGTCTG	GGAGAACTTG	TACATAATGG
730	740	750	760	770	780	790	800
	GCTTTAAATG	ATAATGACTT	TGGTCAAGGA	AGAACAGGTG	GTAGATTTGG	GAAAGTTAAA	GCCCAACAT
810	820	830	840	850	860	870	880
	AGGAGTGCAG	GTGAATGCAA	AGCTAGTCAT	TTCTCACGAA	GAAGAGTTGG	CACCATTGCA	TANATCGATT
890	900	910		930	940	950	960
CCTTCAGATC	CAGAAGAAAG	GAAAAGATAT	GTCATCCCAT	ACCACACCAA	AGCAGCTCAT	TTTGATATAG	ATTGGGGTAA
970	980	990	1000	1010	1020	1030	1040
_	TCCAATCTGT		CTATGAATAT	GGTTATGGCA	GTTGGGAAAT	GATAAAAATG	GATCCTGATC
1050	1060	1070	1080	1090	1100	1110	1120
TCAGTTTGAC	ACAGAAGATT	TTACCTGATG	ATCCAGATAA	GANACCCCAG	GCTAAGCAGT	TACAGACTCG	TGCAGATTAC
1130	1140	1150	1160	1170	1180	1190	1200
CTCATTAAAT	TACTGAATAA	AGACCTTGCA	AGAAAGGAAG	CACAGAGACT	TGCTGGTGCA	GGCAATTCAA	AGAGGAGAAA
1210	1220	1230	1240	1250	1260	1270	1280
	AAGAAGAATA	AAGCAACAAA	GGCTGC		•		
1290	1300	1310					

Figure 9.

	· •
C CHD-1A H CHD-1	DARRYLGRNIGHL*RIASQTHYFENIRSTRKGILDLHLVT*VDFLFNFLILTMNCHSDEE FALCPPVTQREPQETRECRKFIFEILIFEEICIHTHLLIGDFCFINFLIFTMNCHSDEE
C CHD-1A M CHD-1	SVRNSSGESSRSDDDBAGSASGSGSGSGSGSGSGSGSGSGSGSGSESGSGSESESD SVRNGSGESSQSGDD-CGSASGSGSGSGSSSGSSSGSGSGSGSDSGSGSGSGSGSESESD
C CHD-1A M CHD-1	TSREKKQVQAKPPKADGSEFWKSSPSILAVQRSAVLKKQQQQQKAASSDSGSEEDSS TSRENK-VQAKPPKVDGAEFWKSSPSILAVQRSAMLRKQPQQAQQQRPASSNSGSEEDSS
C CHD-1A M CHD-1	SSEDSADDSSSETKKKKHKDEDWOMSGSGSVSGTGSDSESAEDGDKSSCEESESDYEPKN SSEDS-DDSSSGAKKKHNDEDWOMSGSGSPSQLGSDSESEEERDKSSCDGTESDYEPKN
C CHD-1A M CHD-1	KVKSRKPPSRIKPKSGKKSTGOKKROLDSSEZZZDDDZDYDKRGSRROATVNVSYKBAZZ KVRSRKPONRSKSKNGKKILGOKKROIDSSEDZDDZDYDNDKRSSRROATVNVSYKEDZZ **.**** . * *.*.*** *****************
C CED-1A M CED-1	TKTDSDDLLEVCGEDVPQTEBDEFETIEKFHDSRIGRKGATGASTTIYAVEADGDPNAGF HKTDSDDLLEVCGEDVPQPEDEEFETIERVHDCRVGRKGATGATTTIYAVEADGDPNAGF
C CHD-1A M CHD-1	ktxefceiqylikwkgwshihntweteetlkqqnyrghkkldnykkkdqetkrwlknas ekskeigeiqylikwkgwshihntweteetlkqqnykghnkldnykkkdqetkrwlknas ernkefgdiqylikwkgwshihntweteetlkqqnyrghkkldnykkkdqetkrwlknas
BUMAN	PEDVEYYNCQQELTDDLHKQYQIVERTNXSPQSKSAAGYP
C CHD-1A	PEDVEYYNCQQELTDDLHXQYQIVERIIAHSNQKSAAGYPDYYCKHQGLPYSECSWEDGA
M CHD-1	PEDVEYYNCOOELTDDLHKOYOIVERILAHSNOKSAAGLPDYYCKWOGLPYSECSWEDGA
C CHD-1A	LIAKKPOARIDEYFSRNOSKTTPFKDCKVLKORPRFVALKKOPSYIGGEESLELRDYOLN
M CHD-1	LISKKFOTCIDEYFSRNOSKTTPFKDCKVIKORPRFVALKKOPSYIGGEFGLELRDYOLN
C CHD-1A	CI MAI METALECATI MARKET CHEMICALICAI MAI REPRIOT ACTUAL LIBERT CONTROL CONTRO
M CHD-1	GLNWLAHSWCKGNSCILADEMGLGKTIQTISFLNYLFHEHQLYGPFLLRVPLSTLTSWQR GLNWLAHSWCKGNSCILADEMGLGKTIQTISFLNYLFHEHQLYGPFLLVVPLSTLTSWQR

C CHD-1A M CHD-1	EIQTWAPQHNAVVYIGDITSRNHIRTHEWHHPQTRRLKFNILLTTYEILLXDKSFIGGIN EIQTWASQHNAVVYIGDINSRNHIRTHEWHHPQTRRLKFNILLTTYEILLXDKAFIGGIN
	****** ******* ***********************
C CED-1A M CED-1	WAFIGVDEAHRLENDDSLLYRTLIDFKSNHRLLITGTPLONSLELWSLLHFIMPEKFSS WAFIGVDEAHRLENDDSLLYRTLIDFKSNHRLLITGTPLONSLELWSLLHFIMPEKFSS
C CHD-1A M CHD-1	Wedfeeehgkgreygyaslhkelepfllrrvkkdvekslpakveqilrhehsalqkqyyk Wedfeeehgkgreygyaslhkelepfllrrvkkdvekslpakveqilrhehsalqkqyyk
C CHD-1A H CHD-1	WILTRNYKALSKGSKGSTSGFLNIMÆLKKCCNBCYLIKPPDDNEFYNKQZALQHLIRSS WILTRNYKALSKGSKGSTSGFLNIMÆLKKCCNBCYLIKPPDNNEFYNKQZALQHLIRSS
C CHD-1A M CHD-1	GKLILLDKLLIRLRERGNRVLIFSQHVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQAL GKLILLDKLLIRLRERGNRVLIFSQHVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQAL

SUBSTITUTE SHEET (RULE 26)

PCT/GB96/01341

	1
C CED-1A	Defnaegsedfcfilistraggiginlasadtvvifdsdwipondloagaraerigokkov
M CED-1	Defnaegsedfcfilistraggiginlasadtvvifdsdwipondloagaraerigokkov
C CHD-W	-iyrlvtkgsveedilerakkkmvldhlviormdttgktvlhtgstpssstpfnkeelsa
C CHD-1A	niyrlvtkgsveedilerakkkmvldhlviormdttgktvlhtgsapssstpfnkeelsa
M CHD-1	niyrlvtkgsveedilerakkkmvldhlviormdttgktvlhtgstpssstpfnkeelsa
C CHD-W	ILKPGAEELFKEPEXEEEEPQEMDIDEILKRXETRENESGPLTVGDELLSQFKVANPSRM
C CHD-1A	ILKFGAEELFKEPEGEEQEPQEMDIDEILKRAETHENEPGPLSVGDELLSQFKVANPSRM
M CHD-1	ILKFGAEELFKEPEGEEQEPQEMDIDEILKRAETRENEPGPLTVGDELLSQFKVANFSRM
C CHD-W	DEDDIELEPEONLRWEEIIPEVOWRRIEGKEROKELEEIYMLPRWRNCAKOISFNONEG
C CHD-1A	DEDDIELEPERNSKWEEIIPEEORRRLEKEEROKELEEIYMLPRWRNCAKOISFNOSEG
M CHD-1	DEDDIELEPERNSRWEEIIPESORRIEKEEROKELEEIYMLPRWRNCAKOISFNOSEG
C CHD-W	RCSRSRRYSGSDSDSISERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGPVER
C CHD-1A	RRSRSRRYSGSDSDSISERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGPLER
M CHD-1	RRSRSRRYSGSDSDSITERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGPLER
C CHD-W	LDAIARDAELVDKSETDLRRLGELVHNGCIKALNDNDFGQGRTGGRFGKVKGPTFRLAGV
C CHD-1A	LDAIARDAELVDKSETDLRRLGELVHNGCVKALKDSSSGTERAGGRLGKVKGPTFRLSGV
M CHD-1	LDAVARDAELVDKSETDLRRLGELVHNGCIKALKDNSSGQERAGGRLGKVKGPTFRLSGV
C CHD-W	QVNAKLVISHEEBLAPLHKSIPSDPEERKRYVIPYHTKAAHFDIDWGKEDDSNLLIGIYE
C CHD-1A	QVNAKLVIAHEDELIPLHKSIPSDPEERKQTTIPCHTKAAHFDIDWGKEDDSNLLIGIYE
M CHD-1	QVNAKLVISHEEBLAPLHKSIPSDPEERKRYVIPCHTKAAHFDIDWGKEDDSNLLVGIYE
C CHD-N	YGYGSWEHIKHDPDLSLTCKILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAG
C CHD-1A	YGYGSWEHIKHDPDLSLTEKILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKREAQRLCG
M CHD-1	YGYGSWEHIKHDPDLSLTQKILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAG
C CHD-W C CHD-1A M CHD-1	ACNSKRRKTRSKKNKATKAA AGGSKRRKTRAKKSKAMKSIKVKEEIKSDSSPLPSEKSDEDDDKLINDSKPESKDRS AGNSKRRKTRNKKNK-MKASKIKEEIKSDSSPQPSEKSDEDDEEEDNKVNEMKSENKEKS
C CHD-1A	KKSVVSDAPVHITASGEPVPIABESEELDOKTFSICKERMRPVKAALKOLDRPEKGLSER
M CHD-1	KKIPLLDTPVHITATSEPVPISEESEELHOKTFSVCKERMRPVKAALKOLDRPEKGLSER
C CHD-1A	EQLEHTROCLIKIGDHITECLKEYSNPEQIKOWRKNLWIFVSKFTEFDARKLHKLYKHAI
M CHD-1	EQLEHTROCLIKIGDHITECLKEYTNPEQIKOWRKNLWIFVSKFTEFDARKLHKLYKHAI
C CHD-1A M CHD-1	KKRDESQQNSDQN-SNVATTHVIRNPDMERLKENTNHDDSSRDSYSSDRHLSQYHDHHKD KKRDESQQHNDQNISSNVNTHVIRNPDVERLKETTNHDDSSRDSYSSDRHLSQYHDHHKD
C CED-1A	REQGDSYKKSDSRKRPYSSFSNGKDEREWDHYRQDSRYYSDREKERKLDDERSREHRPSL
M CED-1	REQGDAYKKSDSRKRPYSAFSNGKDERDWDHYKQDSRYYSDS-KERKLDDERSRDERSNL
C CHD-1A M CHD-1	EGGLIND-RCHSDHRSHSDHRMHSDHRSTPSTHIINPPRDYRYLSDMOLDHRAASSGPRSP EGNLINDSRGHSDHRSHSDHRIHSDHRSTSEYSHHINSSRDYRYHSDMONDHRASGSGPRSP \$
C CHD-1A M CHD-1	LDQRSPYGSRSPFEHSAEHRSTPEHTWSSRKTXQKLMSLSSGTLFXP LDQRSPYGSRSPLGHRSPFEHSSDHKSTPEHTWSSRKTXQRLTFSGPSFXPYTVNXHSNC
C CHD-1A C CHD-1A C CHD-1A C CHD-1A C CHD-1A C CHD-1A	LTXLERYGLDILSVAVLLLISRHOGLLSQOKKNIFVFKVYAALCCKCCGTFFLRNGRCLL LQGPQBCPFQTGSYYKTLHVKVVLGXTQIKLCLXHNTXTLTCAYVSGKOGFILFYFLVE NSQGLGSLSKATCLHCTLRPPCRFSSQAXIFKFCTYSCKIARISFVCDQLXCLFHKQTNK QKTIKXXNITKPTNOCKLLXINXMSFFPSGFFMLFLSPTTQAFFSQSQYTYHFXXNISHE SECKNGEGNILFHLVLLFYWILLHTGLFYFIFFYXXTVSVVIVVNNSENIPLXTVPHK AFQVHWFKRRKCSIGHFKTQISQDSLXIHLFSLFNHGNNVKCAHQQLIFXKIXHTLLTE LLQCTLIVHRXLLSDKINXLXPKKT
	SUBSTITUTE SHEET (RULE 26)

Figure 10.

	·	
55	KPPKADGSEFWKSSPSILAVORSAVLKKQQQQQKAASSDSGSEEDSSSSE	104
2654	.:: .:. .: .:.: .:: :. : MAAKDISTEVLON.PELYGLRRSHRAAAHQQNYFNDSDDEDDE	2695
105	DSADDSSSETKKKKHKDEDWOMSGSGSVSGTGSDSESAEDGDKSSCEESE	154
2696	DNIKQSRRKRMTTIEDDEDEFEDEEGEEDSGEDEDEEDFEEDD	2738
155	SDYEPKNKVKSRKPPSRIKPKSGKKSTGOKKROLDSSEEEEDDDEDYDKR	204
2739	. : : DYYGSPIKQNRSKPKSRTKSKSKSKPKSQSEKQSTVKIPTRF	2780
205	GSRRQATVNVSYKEAEETKTDSDDLLEVCGEDVPQTEEDEFE	246
2781	:. ::: :: : .: ::: . SNRQNKTVNYNIDYSDDDLLESEDDYGSEEALSEENVEEASANPQPEDFE	2830
247	TIEKFMDSRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKW	296
2831	- : .:: : . .: :::::: :::: GIDIVINERL	2870
297	KGWSHIENTWETEETLKOONVKGMNKLDNYKKKDQETKRWLKNASPE	343
2871	:: : .: : ::: . ::: :: TDESHLHNTWETYESIGQVRGLKRLDNYCKQFIIEDQQVRLDPYVTAE	2918
344	DVEYYNCQQELTDDLHKQYQIVERIIA HSNQKSAAGYPDYYCKWQGLP	391
2919	: .::. .::::. . ::::: . DIEIMDMERERRLDEFEEFEVPERIIDSQRASLEDGTSQLQYLVKWRRLN	2968
392	YSECSWEDGALIAKKFOARIDEYFSRNOSKTTPFKDCKVLKORPRFVALK	441
2969		3018
442	KOPSYIGGHESLELRDYOLNGLNWLAHSWCKGNSCILADEMGLGKTIOTI	491
3019	VQPPFIKGGELRDFQLTGINWMAFLWSKGDNGILADEMGLGKTVQTV	3065
492	SFLNYLFHEHOLYGPFLLRVPLSTLTSWOREIOTWAPOMNAVVYLGDITS	541
3066	. ::: : .:: :: ::. .::. :: ::. : . AFISWLIFARRQNGPHIIVVPLSTMPAWLDTFEKWAPDLNCICYMGNQKS	3115
542	RNMIRTHEWMBPQTKRLKFNILLTTYEILLKDKSFLGGLNWAFIGV	587
3116	RDTIREYEFYTNPRAKGKKTMKFNVLLTTYEYILKDRAELGSIKWQFMAV	3165
588	DEAHRLKNDDSLLYRTLIDFKSNHRLLITGTPLONSLKELWSLLHFIMPE	637
3166	DEAHRLKNAESSLYESLNSFKVANRMLITGTPLQNNIKELAALVNFLMPG	3215
638	KFSSWEDFE.EEHGKGREYGYASLHKELEPFLLRRVKKDVEKSLPAKVEQ	686
3216	: . :::: ::::: : :: : :	3265
687	ILRMEMSALOROYYKWILTRNYKALSKGSKGSTSGFLNIMMELKKCCNEC	736
3266	: : : : : : : : : : : : :	3315
737	YLIKPPDDNEFYNKQEALQHLIRSSGKLILLDKLLIRLRERGN	779
3316	::::::: : : :: :: :: :: :: :	3365

780	RVLIFSOMVRMLDILAEYLKYROFPFORLDGSIKGELRKOALDHFNAEGS	829
3366	RVLIFSQMVRMLDILGDYLSIKGINFQRLDGTVPSAQRRISIDHFNSPDS	341
830	EDFCFLLSTRAGGLGINLASADTVVIFDSDWNPONDLOAQARAHRIGORK	879
3416	NDFVFLLSTRAGGLGINLMTADTVVIFDSDWNPQADLQAMARAERIGQKN	3465
880	QVNIYRLVTKGSVEEDILERAKKKMVLDHLVIQRMDTTGKTVLHTGSTPS : : : : :	929
3466	EVMVYRLVSKDTVEEEVLERARKKMILEYAIISLGVTDGNKYTKKNEP	3513
930	SSTPFNKEELSAILKFGAEELFKEPEGEEQEPQEMDIDEILKRAETRENE	979
3514	NAGELSAILKFGAGNMFTATD.NOKKLEDLNLDDVLNHAEDHVTT	3557
980	PGPLTVGDELLSOFKVANFSNMDEDDIELEPERNSRNWEEIIPESQR	1026
3558	: : : . :: ::	3594
1027	RRIEEEEROKELEEIYMLPRMRNCAKQISFNGSE	1060
3595	KKLQDĖĖQKRKDĖĖ YVKEQLEMMNRRDNALKKIKNSVNGDGTAANSDSDD	3644
1061	GRRSRRYSGSDSDSITERKRPKKRGRPRTIPR.ENIKGFSDAE	1104
3645		3691
1105	IRRFIKSYKKFGGPLERLDAVARDAELVDKSETDLRRLGEL	1145
3692	GTLPVKSFEKYGETYDEMMEAARDCVHEEEKNRKEILEKLEKHATAYRAK	3741
1146	VHNGCIKALKD.NSSGQERAGGRLGKVKGPTFRISGVQ.VNAKLVISHEE : .: : : . : . . : :	1193
3742	LKSGEIKAENOPKONPLTRLSLKKREKKAVLFNFKGVKSLNAESLLSRVE	3791
	ELAPLEKSIPSD.PEERKRYVIPCHTKAAHFDIDWGKEDDSNLLVGIY : : .:: .: .: .: .: .: .: .: .: .: .: .: .	1240
	DLKYLKNLINSNYKDDPLKFSLGNNTPKPVONWSSNWTKEEDEKLLIGVF	3841
	EYGYGSWEMIKMDPDLSLTQKILPDD	1266
3842	KYGYGSWTQIRDDPFLGITDKIFLNEVENPVAKKSASSSDTTPTPSKKGK	3891
1267	PDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAGAGNS	1305
	GITGSSKKVPGAIHLGRRVDYLLSFLRGGLNTKSPSADIGSKKLPTGPSK	
	KRRKTRNKKNKMKASKIKEEIKSDSSPOPSEKSDEDDEEEDNKVNEM	
	RRQRRPANESKSMTPEITSSEPANGPPSKRMKALPKGPAALINNTRLSPN	
1353	KSENKEKSKKIPLLDTPVHITATSEPVPISEESEELHOKTFSVCKERMRP 	1402
	SPTPPLKSKVSRDNGTRQSSNPSSGSAHEKEYDSMDEEDCRHTMSA	
1403	VKAALKOLDRPEKGLSEREQLEHTROCLIKIGDHITECLKEYTNPEQIKQ	1452
	:: . :: : .: : : :: :	4086
1453	WRKNLWIFVSKFTEFDARKLHKLYKHAIKKROESOO 1488 : : : : . . YRKHLWSYSANFWPADVKSTRLMAMYDKITESOK 4120	
4087	YRKHLWSYSANFWPADVKSTKLMAMYDKITESOK 4120	

Figure 11.

CCHD AVEAD GDPNAGFEKSKELGE.IQYLIKWKGWSHIBNTWETEET LKQQNVKGMNKLDNYKK MCHD AVEAD GDPNAGFERNKEPGD.IQYLIKWKGWSHIBNTWETEET LKQQNVRGNKKLDNYKK YCHD EGKVL EKTVPDLNNCKE..N.YEFLIKWTDESHLHNTWETYES IGQ..VRGLKRLDNYCK YAVEKIIDRRVRKGK.VEYYLKWKGYPETENTWEPENN LDCQDLIQQY LDCPELISEF MMOD1 EEEEE YVVEKVLDRRVVKGK.VEYYLKWKGFSEENTWEPENN LDCPELISEF MMOD2 AEPEE FVVEKVLDRRVVKGK.VEYFLKWKGFTDADNTWEPENN LDCPELISEF LDCPELISEF FVVEKVLDRRVVKGK.VEYFLKWKGFTDADNTWEPENN LDCPELIEDF YAAEKIIQKRVKKGV.VEYFLKWKGWNQRYNTWEPENN ILDCRLIEDF YAAEKIIQKRVKKGV.VEYRVKWKGWNQRYNTWEPENN ILDCRLIEDF YAAEKIIQKRVKKGV.VEYRVKWKGWNQRYNTWEPENN ILDCRLIEDF YAAEKIIQKRVKKGV.VEYRVKWKGWNQRYNTWEPENN ILDCRLIEDF YAAEKIIQKRVKKGV.VEYRVKWKGWNQRYNTWEPENN ILDCRLIEDF YAAECILSKRLRKGK.LEYLVKWRGWSSKHNSWEPEEN ILDCRLLLAF

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Figure 12.



Figure 13.

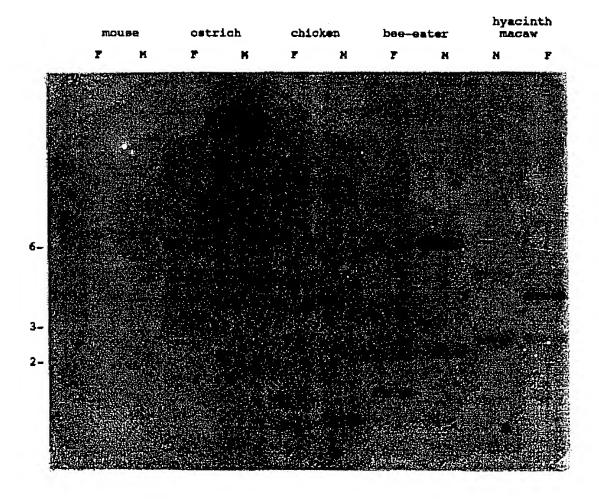
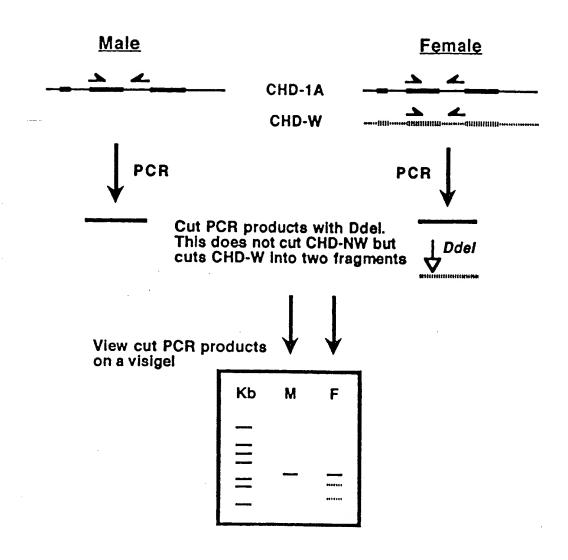


Figure 14.

MOUSE CHICKEN SPIX CHICKEN SPIX HYACINTE P1 P3	CHD-1A CHD-W CHD-W	AGA TAT TCT GGA TCT GAT AGT GAT TCA ATC TCG GAA CC A-A CC CCA CCA CCA A TAT TCT GGA TCT GAT AGT GAY TC AGA TAT TCC GGA TCT GAT AGT GA
MOUSE CHICKEN SPIX CHICKEN SPIX HYACINTH	CHD1 CHD-1A CHD-1A CHD-W CHD-W	AGG AAA CGG CCG AAG AAA CGT GGG CGA CCC CGC ACTA AAGA ATACAAAAAAAAAAA
MOUSE CHICKEN SPIX CHICKEN SPIX P2 BYACINTH BYACINTH	CHD1 CHD-1A CHD-W CHD-W CHD-W CHD-W	ATC CCT CGG GAG AAT ATT AAA GGA TTT AGT GAT GCG GAGTAA

Figure 15.



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Figure 16.

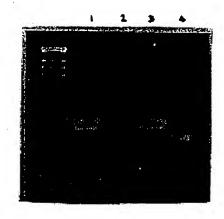


Figure 17.

